

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/530,209

Source: 1638

Date Processed by STIC: 2/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

#100
3/21/01RAW SEQUENCE LISTING
PATENT APPLICATION US/09/530,209DATE: 02/27/2001
TIME: 20:20:22

INPUT SET: S36432.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

See pp. 6-7

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

(1) General Information:

(i) APPLICANT: ↑ move up - all responses must be on same line as heading
 (A) NAME: CropDesign NV
 (B) STREET: TechnologiePark Zwijnaarde 3
 (C) CITY: Gent
 (D) STATE: none
 (E) COUNTRY: Belgium
 (F) POSTAL CODE (ZIP): 9052

delete

(ii) TITLE OF INVENTION: A novel mitogenic cyclin and uses thereof

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(v) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG AGC AAC
 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn

45 1

5

10

15

48

(iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE:
 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

(EPO)

add these
mandatory
headings and
responses for
a U.S. case

FYI: EPO format
is invalid for a
U.S. case

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/530,209DATE: 02/27/2001
TIME: 20:20:22

INPUT SET: S36432.raw

| | | |
|----|---|-----|
| 47 | GTT GAT GAT GAG GGC ATG ATT GTT GAC GAA ACT CCG ATT GAA ATT TCG | 96 |
| 48 | Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser | |
| 49 | 20 25 30 | |
| 50 | | |
| 51 | ATT CCT CAG ATG GGT TTT TCT CAA TCG GAG AGT GAG GAG ATT ATC ATG | 144 |
| 52 | Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met | |
| 53 | 35 40 45 | |
| 54 | | |
| 55 | GAG ATG GTG GAG AAG GAG AAG CAG CAT TTG CCA AGT GAT GAT TAC ATC | 192 |
| 56 | Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile | |
| 57 | 50 55 60 | |
| 58 | | |
| 59 | AAG AGA CTT AGA AGT GGA GAT TTG GAT TTG AAT GTT GGA AGA AGA GAT | 240 |
| 60 | Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp | |
| 61 | 65 70 75 80 | |
| 62 | | |
| 63 | GCC CTC AAT TGG ATT TGG AAG GCT TGT GAA GTA CAC CAG TTT GGA CCA | 288 |
| 64 | Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro | |
| 65 | 85 90 95 | |
| 66 | | |
| 67 | TTG TGT TTT TGC TTA GCA ATG AAC TAC TTG GAT CGA TTC TTA TCG GTT | 336 |
| 68 | Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val | |
| 69 | 100 105 110 | |
| 70 | | |
| 71 | CAT GAT TTG CCT AGT GGC AAA GGT TGG ATA TTG CAG TTG TTG GCT GTG | 384 |
| 72 | His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val | |
| 73 | 115 120 125 | |
| 74 | | |
| 75 | GCT TGT TTA TCA TTG GCA GCC AAA ATT GAA GAA ACT GAA GTT CCA ATG | 432 |
| 76 | Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met | |
| 77 | 130 135 140 | |
| 78 | | |
| 79 | TTG ATA GAT CTT CAG GTT GGA GAT CCT CAG TTT GTG TTT GAG GCT AAA | 480 |
| 80 | Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys | |
| 81 | 145 150 155 160 | |
| 82 | | |
| 83 | TCA GTC CAA AGA ATG GAG CTT TTG GTG TTG AAC AAA TTG AAA TGG AGA | 528 |
| 84 | Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg | |
| 85 | 165 170 175 | |
| 86 | | |
| 87 | TTG AGA GCA ATA ACT CCA TGC TCA TAC ATA AGA TAT TTC CTG AGA AAG | 576 |
| 88 | Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys | |
| 89 | 180 185 190 | |
| 90 | | |
| 91 | ATG AGT AAA TGT GAT CAA GAA CCA TCC AAC ACA TTG ATA TCT AGA TCA | 624 |
| 92 | Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser | |
| 93 | 195 200 205 | |
| 94 | | |
| 95 | TTA CAA GTG ATA GCC AGC ACA ACC AAA GGT ATT GAC TTT TTG GAG TTT | 672 |
| 96 | Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe | |
| 97 | 210 215 220 | |
| 98 | | |
| 99 | AGA CCT TCT GAA GCT GCT GCT GTG GCA CTT TCT GTT TCT GGA GAA | 720 |

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/530,209DATE: 02/27/2001
TIME: 20:20:23

INPUT SET: S36432.raw

100 Arg Pro Ser Glu Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu
101 225 230 235 240
102
103 TTG CAG AGA GTA CAC TTT GAC AAC TCT TCC TTC TCT CCT CTT TTC TCA 768
104 Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
105 245 250 255
106
107 CTA CTT CAA AAG GAG AGA GTG AAG AAG ATA GGG GAA ATG ATA GAG AGT 816
108 Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
109 260 265 270
110
111 GAT GGC TCA GAC TTA TGT TCA CAA ACA CCC AAT GGG GTT TTA GAA GTA 864
112 Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val
113 275 280 285
114
115 TCG GCT TGT TGT TTC AGC TTT AAG ACC CAT GAT TCT TCT TCT TCT TAT 912
116 Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Tyr
117 290 295 300
118
119 ACA CAT CTT TCT TAA 927
120 Thr His Leu Ser *
121 305
122
123
124 (2) INFORMATION FOR SEQ ID NO: 2:
125
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 308 amino acids
128 (B) TYPE: amino acid
129 (D) TOPOLOGY: linear
130
131 (ii) MOLECULE TYPE: protein
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
133
134 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn 768
135 1 5 10 15
136
137 Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser 816
138 20 25 30
139
140 Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met 864
141 35 40 45
142
143 Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile 912
144 50 55 60
145
146 Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp 927
147 65 70 75 80
148
149 Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro 816
150 85 90 95
151
152 Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/530,209DATE: 02/27/2001
TIME: 20:20:23

INPUT SET: S36432.raw

153 100 105 110
154
155 His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val
156 115 120 125
157
158 Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met
159 130 135 140
160
161 Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys
162 145 150 155 160
163
164 Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg
165 165 170 175
166
167 Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys
168 180 185 190
169
170 Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser
171 195 200 205
172
173 Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe
174 210 215 220
175
176 Arg Pro Ser Glu Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu
177 225 230 235 240
178
179 Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
180 245 250 255
181
182 Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
183 260 265 270
184
185 Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val
186 275 280 285
187
188 Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Tyr
189 290 295 300
190
191 Thr His Leu Ser
192 305
193
194
195 (2) INFORMATION FOR SEQ ID NO: 3:
196
197 (i) SEQUENCE CHARACTERISTICS:
198 (A) LENGTH: 24
199 (B) TYPE: nucleic acid
200 (C) STRANDEDNESS: single
201 (D) TOPOLOGY: linear
202
203 (ii) MOLECULE TYPE: other nucleic acid
204 (A) DESCRIPTION: /desc = "oligonucleotide"
205

INPUT SET: S36432.raw

206 (iii) HYPOTHETICAL: YES
207
208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
209
210 GAACACTCGA GTGTAATGGC AGAGG 25
211
212
213
214 (2) INFORMATION FOR SEQ ID NO: 4:
215
216 (i) SEQUENCE CHARACTERISTICS:
217 (A) LENGTH: 25
218 (B) TYPE: nucleic acid
219 (C) STRANDEDNESS: single
220 (D) TOPOLOGY: linear
221
222 (ii) MOLECULE TYPE: other nucleic acid
223 (A) DESCRIPTION: /desc = "oligonucleotide"
224
225 (iii) HYPOTHETICAL: YES
226
227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
228
229 CATCATACTA GTTATAATAA TGTAAG 26
230

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

308
 (see next page)

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn
 1 5 10 15

Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser
 20 25 30

Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met
 35 40 45

Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile
 50 55 60

Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp
 65 70 75 80

Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro
 85 90 95

Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val
 100 105 110

His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val
 115 120 125

Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met
 130 135 140

Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys
 145 150 155 160

Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg
 165 170 175

Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys
 180 185 190

Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser
 195 200 205

Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe
 210 215 220

Arg Pro Ser Glu Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu
 225 230 235 240

Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser
 245 250 255

Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser
 260 265 270

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Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val
275 280 285

Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr
290 295 300

Thr His Leu Ser
305

**) delete ending stop codon*

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/530,209

DATE: 02/27/2001
TIME: 20:20:24

INPUT SET: S36432.raw

| Line | Error | Original Text |
|------|--|--|
| 5 | Mandatory Value Not Present | (i) APPLICANT: |
| 6 | Unknown or Misplaced Identifier | (A) NAME: CropDesign NV |
| 7 | Unknown or Misplaced Identifier | (B) STREET: TechnologiePark Zwijnaarde 3 |
| 8 | Unknown or Misplaced Identifier | (C) CITY: Gent |
| 9 | Unknown or Misplaced Identifier | (D) STATE: none |
| 10 | Unknown or Misplaced Identifier | (E) COUNTRY: Belgium |
| 11 | Unknown or Misplaced Identifier | (F) POSTAL CODE (ZIP): 9052 |
| 195 | Stop Codon at end of sequence removed - no error | (2) INFORMATION FOR SEQ ID NO: 3: |

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION **US/09/530,209**

DATE: 02/27/2001
TIME: 20:20:24

INPUT SET: S36432.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA